```
RESULT 10
AF022889
LOCUS
            AF022889
                                    6240 bp
                                               mRNA
                                                       linear ROD 30
AUG-1998
DEFINITION Mus musculus latent TGF beta binding protein (LTBP-1) mRNA,
            complete cds.
ACCESSION
            AF022889
VERSION
            AF022889.1 GI:3493175
KEYWORDS
SOURCE
            Mus musculus.
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Mus.
           1 (bases 1 to 6240)
REFERENCE
  AUTHORS
            Noquera, I., Cowin, P. and Rifkin, D.B.
            Direct Submission
  JOURNAL
            Submitted (04-SEP-1997) Cell Biology, New York University
Medical
            Center, 550 First Ave, New York, NY 10016, USA
FEATURES
                     Location/Qualifiers
                     1. .6240
     source
                     /organism="Mus musculus"
                     /strain="BALB/c"
                     /db xref="taxon:10090"
                     /tissue type="heart"
                     1. .6240
     gene
                     /gene="LTBP-1"
     5'UTR
                     1. .322
                     /gene="LTBP-1"
     CDS
                     323. .5464
                     /gene="LTBP-1"
                     /codon start=1
                     /product="latent TGF beta binding protein"
                     /protein id="AAC33307.1"
                     /db xref="GI:3493176"
```

/translation="MAGAWLRWGLLLWAGLLAWSAHGRVRRITYVVRPGPGLPAGALP
LAGPPRTFNVALDARYSRSSTAASSRALAGPPAERTRRTSQPGGAALPGLRSPLPPEP
ARPGGPSRQLHSKAGAQTAVTRFAKHGRQVVRSQVQQDAQSAGGSRLQVQQKQQLQGI
NVCGGQCCHGWSKPPGSQRCTKPSCVPPCQNGGMCLRPQLCVCKPGSKGKACEITAAQ
DTMPPAFGGQNPGSSWAPLEQAAKHTSTKKADTLPRVSPVAQMTLTLKPKPSMGLSQQ
IHPQVAPLSSQNVMIRHGQTQEYLLKPKYFPAPKVVSAEQSTEGSFSLRYGQEQGTAP
FQVSNHTGRIKVVFTPSICKVTCTKGNCQNSCQKGNTTTLISENGHAADTLTATNFRV
VICHLPCMNGGQCSSRDKCQCPPNFTGKLCQIPVLGASMPKLYQHAQQQGKALGSHVI
HSTHTLPLTMTSQQGVKVKFPPNIVNIHVKHPPEASVQIHQVSRIDSPGGQKVKETQP
GQSQFSYQGLPVQKTQTVHSTYSHQQLIPHVYPVAAKTQLGRCFQETIGSQQCGKALP
GLSKQEDCCGTVGTSWGFNKCQKCPKKQSYHGYTQMMECLQGYKRVNNTFCQDINECQ
LQGVCPNGECLNTMGSYRCSCKMGFGPDPTFSSCVPDPPVISEEKGPCYRLVSPGRHC

MHPLSVHLTKOICCCSVGKAWGPHCEKCPLPGTAAFKEICPGGMGYTVSGVHRRRPIH QHIGKEAVYVKPKNTQPVAKSTHPPPLPAKEEPVEALTSSWEHGPRGAEPEVVTAPPE KEIPSLDQEKTRLEPGQPQLSPGVSTIHLHPQFPVVVEKTSPPVPVEVAPEASTSSAS QVIAPTQVTEINECTVNPDICGAGHCINLPVRYTCICYEGYKFSEQLRKCVDIDECAQ VRHLCSQGRCENTEGSFLCVCPAGFMASEEGTNCIDVDECLRPDMCRDGRCINTAGAF RCEYCDSGYRMSRRGYCEDIDECLKPSTCPEEQCVNTPGSYQCVPCTEGFRGWNGQCL DVDKCLOPKVCTNGSCTNLEGSYMCSCHRGYSPTPDHRHCQDIDECQQGNLCMNGQCR NTDGSFRCTCGQGYQLSAAKDQCEDIDECEHHHLCSHGQCRNTEGSFQCVCNQGYRAS VLGDHCEDINECLEDSSVCQGGDCINTAGSYDCTCPDGFQLNDNKGCQDINECAQPGL CGSHGECLNTQGSFHCVCEQGFSISADGRTCEDIDECVNNTVCDSHGFCDNTAGSFRC  $\verb|LCYQGFQAPQDGQGCVDVNECELLSGVCGEAFCENVEGSFLCVCADENQEYSPMTGQC|$ RSRVTEDSGVDRQPREEKKECYYNLNDASLCDNVLAPNVTKQECCCTSGAGWGDNCEI FPCPVOGTAEFTEMCPRGKGLVPAGESSYDTGGENYKDADECLLFGEEICKNGYCLNT OPGYECYCKOGTYYDPVKLQCFDMDECQDPNSCIDGQCVNTEGSYNCFCTHPMVLDAS EKRCVOPTESNEQIEETDVYQDLCWEHLSEEYVCSRPLVGKQTTYTECCCLYGEAWGM QCALCPMKDSDDYAQLCNIPVTGRRRPYGRDALVDFSEQYGPETDPYFIQDRFLNSFE ELQAEECGILNGCENGRCVRVQEGYTCDCFDGYHLDMAKMTCVDVNECSELNNRMSLC

```
KNAKCINTEGSYKCLCLPGYIPSDKPNYCTPLNSALNLDKESDLN"

3'UTR 5465..6240

/gene="LTBP-1"

BASE COUNT 1545 a 1639 c 1670 g 1386 t

ORIGIN
```

```
Query Match 87.5%; Score 44.6; DB 10; Length 6240; Best Local Similarity 92.2%; Pred. No. 1.1e-06; Matches 47; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```